

[Additional file 1: Supplementary Tables](#)

Genomic dissection of maternal, additive and non-additive genetic effects for growth and carcass traits in Nile tilapia

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**Table S1:** Number of animals genotyped in different full-sib families.

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
1	P				5	9		30		5	5	26	26		34		15	35	
	G																		
2	P	30	20	18			11		33					9		3			16
	G	30	20	18			11							8					
3	P	29	18	25			6		36					8		13			36
	G																		
4	P	13	7	19			6		23					11		6			14
	G																		
5	P							6		8	7	20	12		25		10	27	
	G							6		8	7	20			21		10	27	
6	P				3	6		46		8	4	39	44		59		17	54	
	G							41		8	4	39			38		17	44	
7	P	32	9	17			8		32					7		2			30
	G	32	9	17			8							7					
8	P				5	3		24		9	3	13	13		19		8	16	
	G							25		8	3	13			10		8	16	
9	P	29	16	26			9		37					11		3			27
	G	29	15	26			9							11					
10	P	35	27	16			8		38					17		6			30
	G																		
11	P				1	2		13		2	1	8	13		22		8	21	
	G																		
12	P				4	2		36		4	3	10	30		47		10	52	
	G							36		4	3	10			34		8	43	
13	P	19	3	14			3		19					7		1			10
	G	19	3	14			3							7					
14	P				2	6		14				16	13		15		12	45	
	G							14				16			9		12	43	
15	P	16	15	22			6		28					12		4			29
	G	16	15	20			6		1					12					
16	P	22	13	17			4		26					15		3			17
	G	22	13	17			5		1					16					1
17	P					4		17		4	6	17	17		34		7	4	
	G																		
18	P							14		6	3	12	22		15		8	18	
	G							14		6	3	12	1		13		7	17	

The rows with P and G denote the total number of phenotyped (coded black) and genotyped animals (coded blue) respectively from each full-sib family. Parents are coded from 1 to 18 in the header rows and columns. Empty cells mean no phenotypes or genotypes were available for that full-sib family.

**Table S2:** Descriptive statistics for the six traits.

	<b>N</b>	<b>Unit</b>	<b>Min</b>	<b>Max</b>	<b>Median</b>	<b>Mean (SE)</b>	<b>SD</b>	<b>CV%</b>
<b>BWH</b>	1119	g	115.60	802.80	390.20	407.31 (3.84)	128.44	31.53
<b>BL</b>	1119	cm	14.10	28.00	22.40	22.38 (0.07)	2.25	10.05
<b>BD</b>	1119	cm	5.00	12.00	8.80	8.89 (0.03)	1.03	11.58
<b>BT</b>	1119	mm	12.90	59.70	40.50	40.70 (0.14)	4.55	11.17
<b>FW</b>	1119	g	20.10	342.60	136.60	143.83 (1.56)	52.32	36.38
<b>FY</b>	1119	%	15.24	50.53	33.15	32.83 (0.09)	3.13	9.54

N is the number of observations having both phenotypes and genotypes, SD is the standard deviation, SE is the standard error and CV is the coefficient of variation expressed as percentage.

**Table S3:** Mean values of the genomic relationship matrices constructed with NOIA and HWE approaches.

	<b>HWE</b>			<b>NOIA</b>		
	<b>Overall</b>	<b>Diagonal</b>	<b>Off-diagonal</b>	<b>Overall</b>	<b>Diagonal</b>	<b>Off-diagonal</b>
<b>G</b>	0.000790	0.8847333	-0.000791354	0.000893	1	-0.000894454
<b>D</b>	0.038489	0.9250984	0.036903020	0.000893	1	-0.000894454
<b>k(G#G)</b>	0.009216	0.7868253	0.007825131	0.011713	1	0.009945195
<b>k(G#D)</b>	0.002971	0.8211928	0.001507525	0.003311	1	0.001528032
<b>k(D#D)</b>	0.005130	0.8581108	0.003604039	0.004223	1	0.002441192

All relationship matrices are calculated from the 1119 individuals in the study population.

**Table S4:** Transformation of the variances on a similar scale based on the relationship matrices.

Traits	Assumption	$\sigma^2_A$	SE	$\sigma^2_{A^*}$	SE	$h^2$	SE	$h^{2^*}$	SE
<b>BWH</b>	<b>NOIA</b>	1242	300	1241	300	0.18	0.04	0.19	0.04
	<b>HWE</b>	1404	339	1241	300	0.20	0.04	0.19	0.04
	<b>Ped</b>	3489	1391	2527	1007	0.44	0.14	0.36	0.10
<b>BD</b>	<b>NOIA</b>	0.13	0.03	0.13	0.03	0.24	0.04	0.24	0.04
	<b>HWE</b>	0.14	0.03	0.13	0.03	0.27	0.05	0.24	0.04
	<b>Ped</b>	0.31	0.12	0.23	0.09	0.50	0.15	0.42	0.11
<b>BL</b>	<b>NOIA</b>	0.40	0.12	0.40	0.12	0.13	0.04	0.13	0.04
	<b>HWE</b>	0.46	0.14	0.40	0.12	0.14	0.04	0.13	0.03
	<b>Ped</b>	1.20	0.50	0.87	0.36	0.33	0.12	0.26	0.08
<b>FW</b>	<b>NOIA</b>	177	47	177	47	0.15	0.04	0.16	0.04
	<b>HWE</b>	200	53	177	47	0.17	0.04	0.16	0.04
	<b>Ped</b>	536	215	388	156	0.39	0.13	0.32	0.09
<b>BT</b>	<b>NOIA</b>	1.70	0.44	1.69	0.44	0.17	0.04	0.18	0.04
	<b>HWE</b>	1.92	0.50	1.69	0.44	0.19	0.04	0.18	0.04
	<b>Ped</b>	1.83	0.92	1.32	0.67	0.18	0.08	0.14	0.06
<b>FY</b>	<b>NOIA</b>	1.76	0.41	1.76	0.41	0.19	0.04	0.19	0.04
	<b>HWE</b>	1.99	0.46	1.76	0.41	0.21	0.04	0.19	0.04
	<b>Ped</b>	2.65	1.17	1.92	0.85	0.26	0.10	0.21	0.07

The additive genetic variance ( $\sigma^2_A$ ) and the heritability ( $h^2$ ) were obtained from the A model, but with no individual homozygosity fitted. The transformed variances and ratio are marked by \*, and were obtained from scaling estimates by  $(\overline{\text{diag}(\mathbf{V})} - \bar{\mathbf{V}})$  of the corresponding relationship matrix  $\mathbf{V}$  (see Table S3) as per [1]. In “Ped”, the genomic relationship matrix was replaced by the numerator relationship matrix obtained from 3 generations of pedigree ( $\mathbf{A}$ ).  $\bar{\mathbf{A}}$  and  $\overline{\text{diag}(\mathbf{A})}$  for the 1119 individuals in the study population were 0.2757587 and 1 respectively.

Literature cited:

1. Legarra A. Comparing estimates of genetic variance across different relationship models. *Theor Popul Biol.* Elsevier; 2016;107:26–30.